

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/252,491DATE: 06/16/94
TIME: 11:12:03

INPUT SET: S3069.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Holly, Richard D
Lok, Si
Foster, Donald C
Hagen, Frederick S
Kaushansky, Kenneth
Kuijper, Joseph L
Lofton-Day, Catherine E
Oort, Pieter J
Burkhead, Steven K

ENTERED

(ii) TITLE OF INVENTION: HEMATOPOIETIC PROTEIN AND MATERIALS AND
METHODS FOR MAKING IT

(iii) NUMBER OF SEQUENCES: 29

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 4225 Roosevelt Way, N.E.
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98105

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E
(B) REGISTRATION NUMBER: 31-648
(C) REFERENCE/DOCKET NUMBER: 93-12C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-547-8080 ext 322
(B) TELEFAX: 206-547-2329

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/252,491DATE: 06/16/94
TIME: 11:12:08

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47
48
49 (2) INFORMATION FOR SEQ ID NO:1:
50
51 (i) SEQUENCE CHARACTERISTICS:
52 (A) LENGTH: 1486 base pairs
53 (B) TYPE: nucleic acid
54 (C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear
56
57 (ii) MOLECULE TYPE: cDNA
58
59
60 (vii) IMMEDIATE SOURCE:
61 (B) CLONE: 1081
62
63 (ix) FEATURE:
64 (A) NAME/KEY: CDS
65 (B) LOCATION: 105..1241
66
67
68 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
69
70 CCTCGTGCCG GTCCTGAGGC CTTTCTCCAC CCGACAGAG TCCTTGGCCC ACCTCTCTCC 60
71
72 CACCCGACTC TGCCGAAAGA AGCACAGAAG CTCAAGCCGC CTCC ATG GCC CCA GGA 116
73 Met Ala Pro Gly
74 1
75
76 AAG ATT CAG GGG AGA GGC CCC ATA CAG GGA GCC ACT TCA GTT AGA CAC 164
77 Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr Ser Val Arg His
78 5 10 15 20
79
80 CTG GCC AGA ATG GAG CTG ACT GAT TTG CTC CTG GCG GCC ATG CTT CTT 212
81 Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala Ala Met Leu Leu
82 25 30 35
83
84 GCA GTG GCA AGA CTA ACT CTG TCC AGC CCC GTA GCT CCT GCC TGT GAC 260
85 Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala Pro Ala Cys Asp
86 40 45 50
87
88 CCC AGA CTC CTA AAT AAA CTG CTG CGT GAC TCC CAC CTC CTT CAC AGC 308
89 Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His Leu Leu His Ser
90 55 60 65
91
92 CGA CTG AGT CAG TGT CCC GAC GTC GAC CCT TTG TCT ATC CCT GTT CTG 356
93 Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser Ile Pro Val Leu
94 70 75 80
95
96 CTG CCT GCT GTG GAC TTT AGC CTG GGA GAA TGG AAA ACC CAG ACG GAA 404
97 Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Thr Glu
98 85 90 95 100
99

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100	CAG AGC AAG GCA CAG GAC ATT CTA GGG GCA GTG TCC CTT CTA CTG GAG	452
101	Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser Leu Leu Leu Glu	
102	105 110 115	
103		
104	GGA GTG ATG GCA GCA CGA GGA CAG TTG GAA CCC TCC TGC CTC TCA TCC	500
105	Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser Cys Leu Ser Ser	
106	120 125 130	
107		
108	CTC CTG GGA CAG CTT TCT GGG CAG GTT CGC CTC CTC TTG GGG GCC CTG	548
109	Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu	
110	135 140 145	
111		
112	CAG GGC CTC CTA GGA ACC CAG CTT CCT CTA CAG GGC AGG ACC ACA GCT	596
113	Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly Arg Thr Thr Ala	
114	150 155 160	
115		
116	CAC AAG GAC CCC AAT GCC CTC TTC TTG AGC TTG CAA CAA CTG CTT CGG	644
117	His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln Gln Leu Leu Arg	
118	165 170 175 180	
119		
120	GGA AAG GTG CGC TTC CTG CTT CTG GTA GAA GGT CCC ACC CTC TGT GTC	692
121	Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro Thr Leu Cys Val	
122	185 190 195	
123		
124	AGA CGG ACC CTG CCA ACC ACA GCT GTC CCA AGC AGT ACT TCT CAA CTC	740
125	Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser Thr Ser Gln Leu	
126	200 205 210	
127		
128	CTC ACA CTA AAC AAG TTC CCA AAC AGG ACT TCT GGA TTG TTG GAG ACG	788
129	Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr	
130	215 220 225	
131		
132	AAC TTC AGT GTC ACA GCC AGA ACT GCT GGC CCT GGA CTT CTG AGC AGG	836
133	Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly Leu Leu Ser Arg	
134	230 235 240	
135		
136	CTT CAG GGA TTC AGA GTC AAG ATT ACT CCT GGT CAG CTA AAT CAA ACC	884
137	Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln Leu Asn Gln Thr	
138	245 250 255 260	
139		
140	TCC AGG TCC CCA GTC CAA ATC TCT GGA TAC CTG AAC AGG ACA CAC GGA	932
141	Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn Arg Thr His Gly	
142	265 270 275	
143		
144	CCT GTG AAT GGA ACT CAT GGG CTC TTT GCT GGA ACC TCA CTT CAG ACC	980
145	Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr Ser Leu Gln Thr	
146	280 285 290	
147		
148	CTG GAA GCC TCA GAC ATC TCG CCC GGA GCT TTC AAC AAA GGC TCC CTG	1028
149	Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn Lys Gly Ser Leu	
150	295 300 305	
151		
152	GCA TTC AAC CTC CAG GGT GGA CTT CCT CCT TCT CCA AGC CTT GCT CCT	1076

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153  Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro Ser Leu Ala Pro
154      310                      315                      320
155
156  GAT GGA CAC ACA CCC TTC CCT CCT TCA CCT GCC TTG CCC ACC ACC CAT      1124
157  Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu Pro Thr Thr His
158  325                      330                      335                      340
159
160  GGA TCT CCA CCC CAG CTC CAC CCC CTG TTT CCT GAC CCT TCC ACC ACC      1172
161  Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp Pro Ser Thr Thr
162      345                      350                      355
163
164  ATG CCT AAC TCT ACC GCC CCT CAT CCA GTC ACA ATG TAC CCT CAT CCC      1220
165  Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met Tyr Pro His Pro
166      360                      365                      370
167
168  AGG AAT TTG TCT CAG GAA ACA TAGCGCGGGC ACTGGCCCAG TGAGCGTCTG      1271
169  Arg Asn Leu Ser Gln Glu Thr
170      375
171
172  CAGCTTCTCT CGGGGACAAG CTTCCCCAGG AAGGCTGAGA GGCAGCTGCA TCTGCTCCAG      1331
173
174  ATGTTCTGCT TTCACCTAAA AGGCCCTGGG GAAGGGATAC ACAGCACTGG AGATTGTAAA      1391
175
176  ATTTTAGGAG CTATTTTTTTT TTAACCTATC AGCAATATTC ATCAGAGCAG CTAGCGATCT      1451
177
178  TTGGTCTATT TTCGGTATAA ATTTGAAAAT CACTA      1486
179
180
181  (2) INFORMATION FOR SEQ ID NO:2:
182
183      (i) SEQUENCE CHARACTERISTICS:
184          (A) LENGTH: 379 amino acids
185          (B) TYPE: amino acid
186          (D) TOPOLOGY: linear
187
188      (ii) MOLECULE TYPE: protein
189
190      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
191
192  Met Ala Pro Gly Lys Ile Gln Gly Arg Gly Pro Ile Gln Gly Ala Thr
193      1          5          10          15
194
195  Ser Val Arg His Leu Ala Arg Met Glu Leu Thr Asp Leu Leu Leu Ala
196      20          25          30
197
198  Ala Met Leu Leu Ala Val Ala Arg Leu Thr Leu Ser Ser Pro Val Ala
199      35          40          45
200
201  Pro Ala Cys Asp Pro Arg Leu Leu Asn Lys Leu Leu Arg Asp Ser His
202      50          55          60
203
204  Leu Leu His Ser Arg Leu Ser Gln Cys Pro Asp Val Asp Pro Leu Ser
205      65          70          75          80

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206
207   Ile Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys
208                               85                      90                      95
209
210   Thr Gln Thr Glu Gln Ser Lys Ala Gln Asp Ile Leu Gly Ala Val Ser
211                               100                      105                      110
212
213   Leu Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Glu Pro Ser
214                               115                      120                      125
215
216   Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu
217                               130                      135                      140
218
219   Leu Gly Ala Leu Gln Gly Leu Leu Gly Thr Gln Leu Pro Leu Gln Gly
220   145                      150                      155                      160
221
222   Arg Thr Thr Ala His Lys Asp Pro Asn Ala Leu Phe Leu Ser Leu Gln
223                               165                      170                      175
224
225   Gln Leu Leu Arg Gly Lys Val Arg Phe Leu Leu Leu Val Glu Gly Pro
226                               180                      185                      190
227
228   Thr Leu Cys Val Arg Arg Thr Leu Pro Thr Thr Ala Val Pro Ser Ser
229                               195                      200                      205
230
231   Thr Ser Gln Leu Leu Thr Leu Asn Lys Phe Pro Asn Arg Thr Ser Gly
232   210                      215                      220
233
234   Leu Leu Glu Thr Asn Phe Ser Val Thr Ala Arg Thr Ala Gly Pro Gly
235   225                      230                      235                      240
236
237   Leu Leu Ser Arg Leu Gln Gly Phe Arg Val Lys Ile Thr Pro Gly Gln
238                               245                      250                      255
239
240   Leu Asn Gln Thr Ser Arg Ser Pro Val Gln Ile Ser Gly Tyr Leu Asn
241                               260                      265                      270
242
243   Arg Thr His Gly Pro Val Asn Gly Thr His Gly Leu Phe Ala Gly Thr
244                               275                      280                      285
245
246   Ser Leu Gln Thr Leu Glu Ala Ser Asp Ile Ser Pro Gly Ala Phe Asn
247   290                      295                      300
248
249   Lys Gly Ser Leu Ala Phe Asn Leu Gln Gly Gly Leu Pro Pro Ser Pro
250   305                      310                      315                      320
251
252   Ser Leu Ala Pro Asp Gly His Thr Pro Phe Pro Pro Ser Pro Ala Leu
253                               325                      330                      335
254
255   Pro Thr Thr His Gly Ser Pro Pro Gln Leu His Pro Leu Phe Pro Asp
256                               340                      345                      350
257
258   Pro Ser Thr Thr Met Pro Asn Ser Thr Ala Pro His Pro Val Thr Met

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SEQUENCE VERIFICATION REPORT
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Original Text